

Compd #	MOLSTRUCTURE
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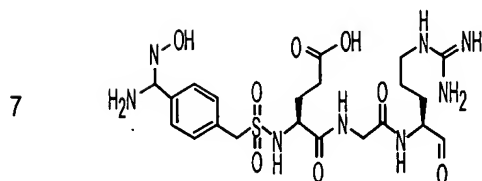


FIG. 1A



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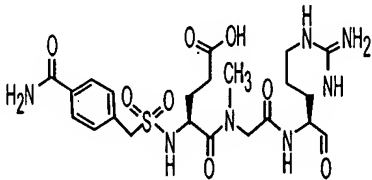
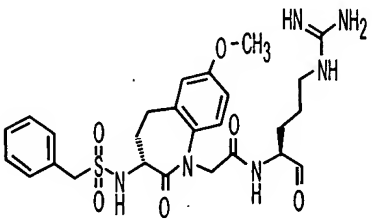
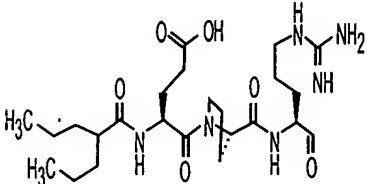
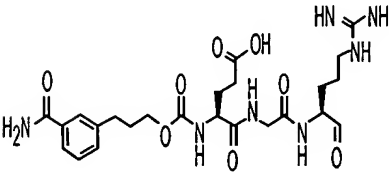
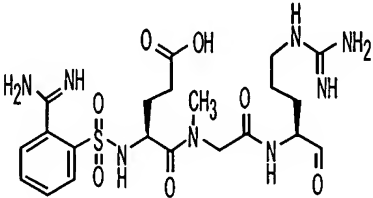
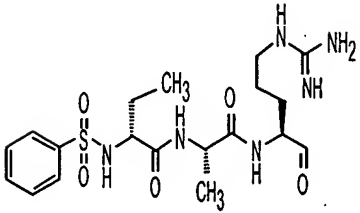
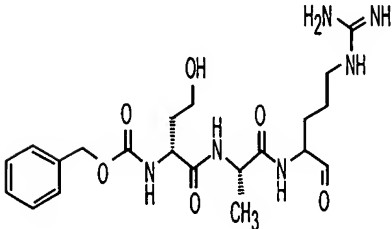
Compd #	MOLSTRUCTURE
8	
9	
10	
11	
12	
13	
14	

FIG. 1B

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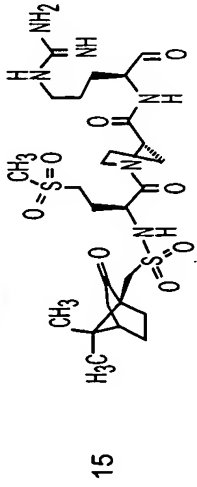
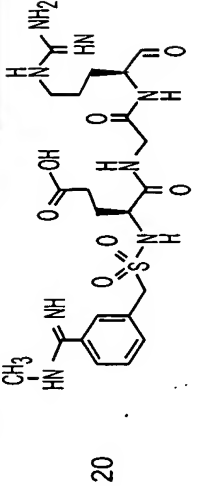
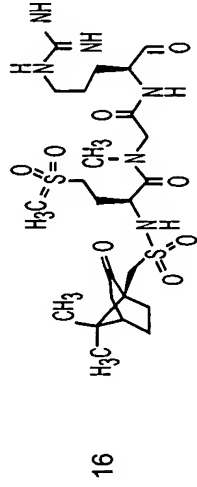
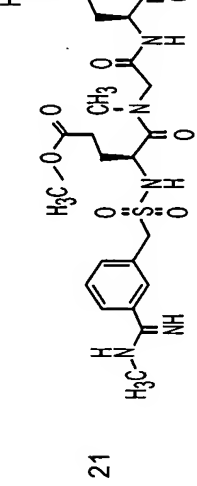
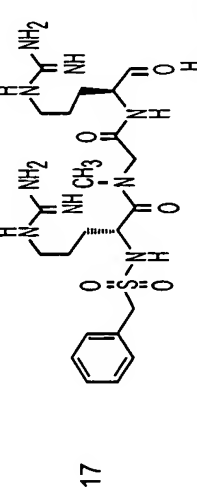
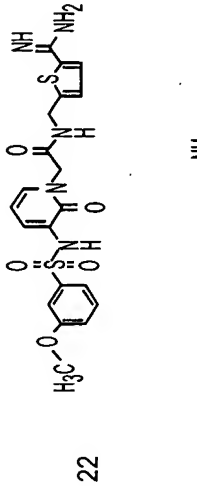
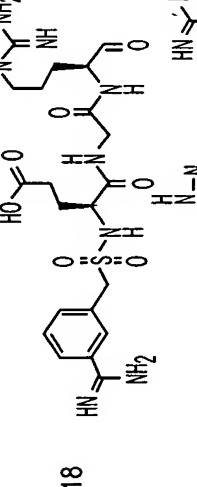
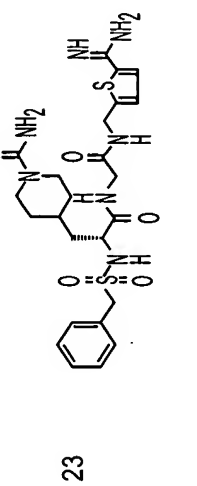
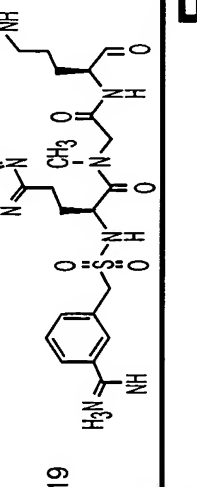
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIG. 1C

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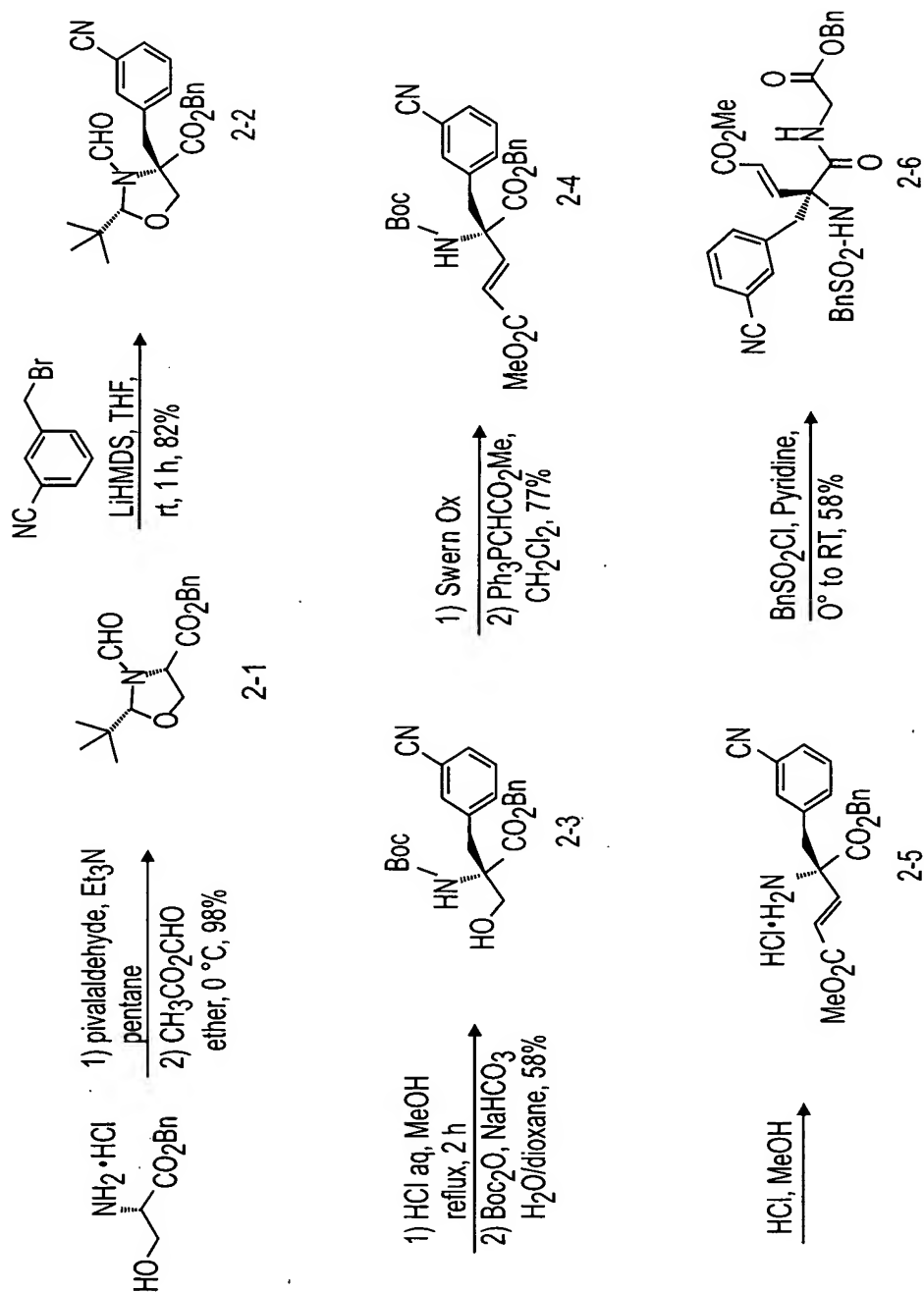


FIG. 2A

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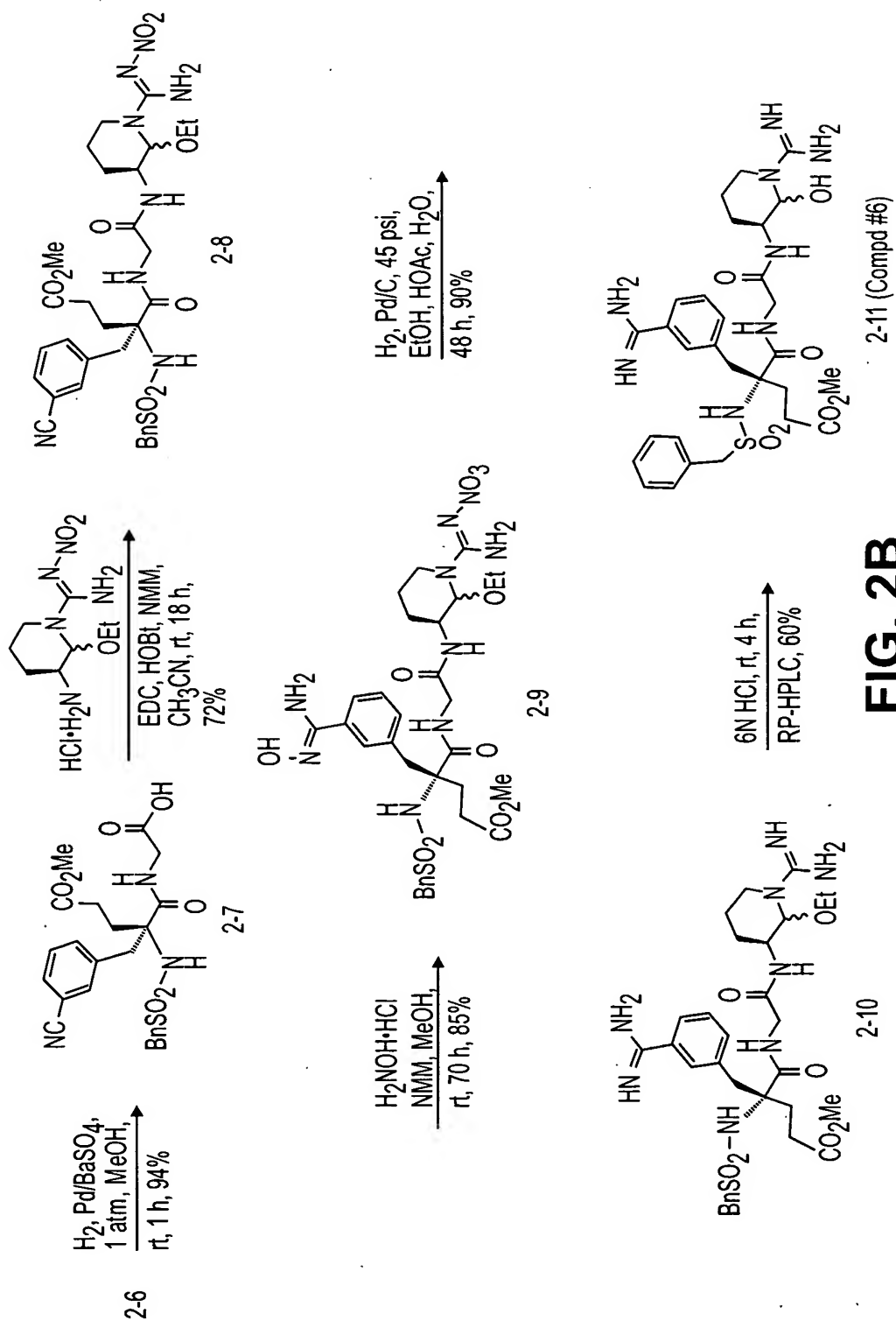


FIG. 2B

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10	20	30	40	50	60
GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT					
CAACAACCCCCGTGCCTACGCCTACTCCCGCTCACCGGGACCGTCCATTTCGGACGTACGA					
V V G G T D A D E G E H P W Q V S L H A>					
70	80	90	100	110	120
CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC					
GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG					
L G Q G H I C G A S L I S P N W L V S A>					
130	140	150	160	170	180
GCACACTGCTACATCGATGACAGAGGATTTCAGGTACTCAGACCCACGCAGTGGACGGCC					
CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCCTCACCTGCCGG					
A H C Y I D D R G F R Y S D P T Q W T A>					
190	200	210	220	230	240
TTCCTGGGCTTGACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC					
AAGGACCCGAACGTGCTGGTCTCGGTTCGCTCGCGGGGACCCACGTCCTCGCGTCCGAG					
F L G L H D Q S Q R S A P G V Q E R R L>					
250	260	270	280	290	300
AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG					
TTCGCGTAGTAGAGGGTGGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC					
K R I I S H P F F N D F T F D Y D I A L>					
310	320	330	340	350	360
CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC					
GACCTCGACCTCTTTGGCCGTCTCATGTGCGAGGTACCACGCCGGGTAGACGGACGGCCTG					
L E L E K P A E Y S S M V R P I C L P D>					

FIG. 3A

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      370      380      390      400      410      420
GCCTCCCATGTCTTCCCTGCCGGAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG
CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC
A S H V F P A G K A I W V T G W G H T Q>

      430      440      450      460      470      480
TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC
ATACCTCCGTGACCGCGCGACTAGGACGTTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG
Y G G T G A L I L Q K G E I R V I N Q T>

      490      500      510      520      530      540
ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC
TGGACGCTCTTGGAGGACGGCGTCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG
T C E N L L P Q Q I T P R M M C V G F L>

      550      560      570      580      590      600
AGCGGCGGCGTGGAATCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG
TCGCCGCCGCACCTGAGGACGGTCCCCTAAGGCCCCCTGGGGACAGGTGCGACCTCCGC
S G G V D S C Q G D S G G P L S S V E A>

      610      620      630      640      650      660
GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC
CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG
D G R I F Q A G V V S W G D G C A Q R N>

      670      680      690      700      710      720
AAGCCAGGCGGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACTGGG
TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTCTGTGACCC
K P G V Y T R L P L F R D W I K E N T G>

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FIG. 3B

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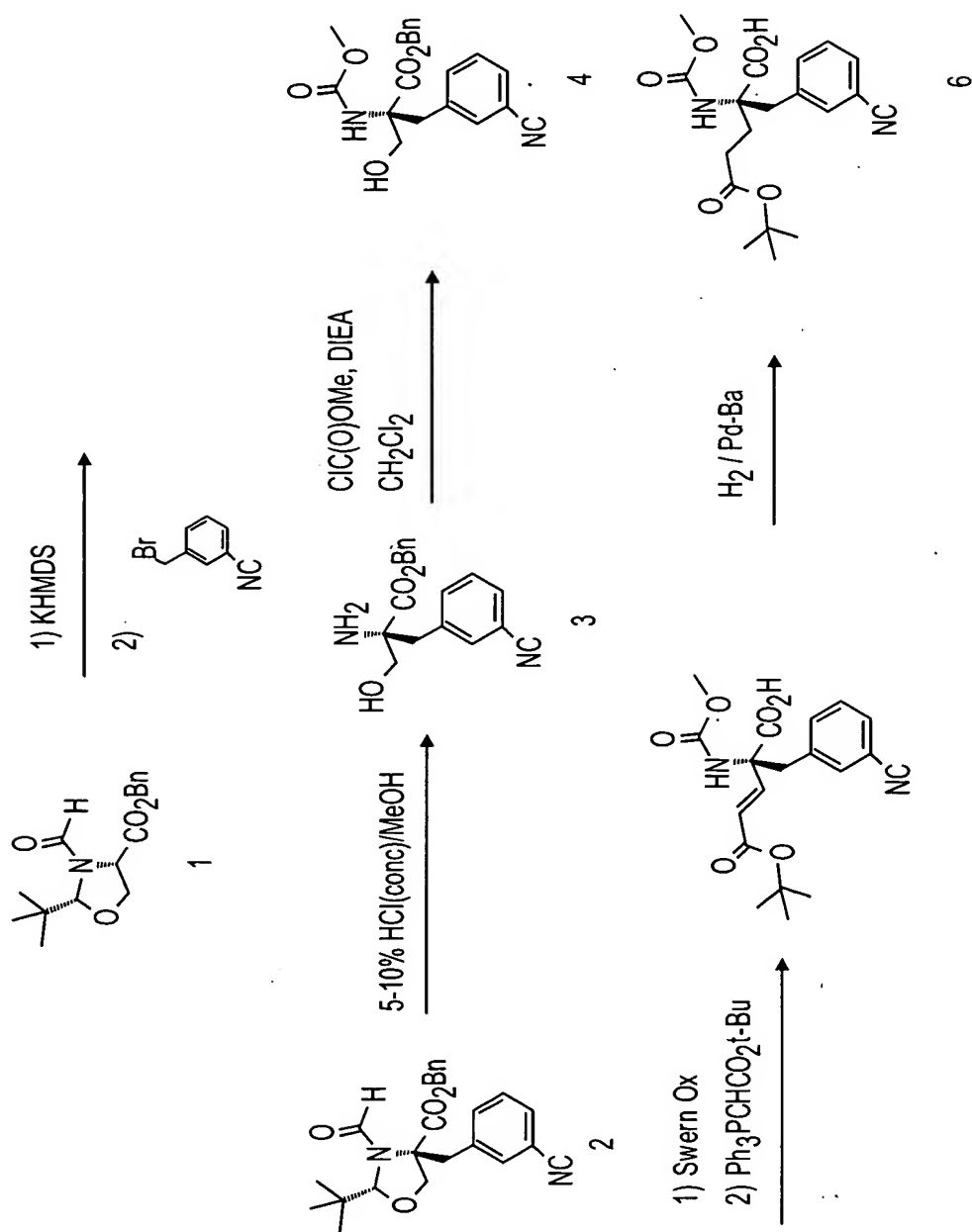
GTATAG

CATATC

V *>

FIG. 3C

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FIG. 4A

6

4

3

1

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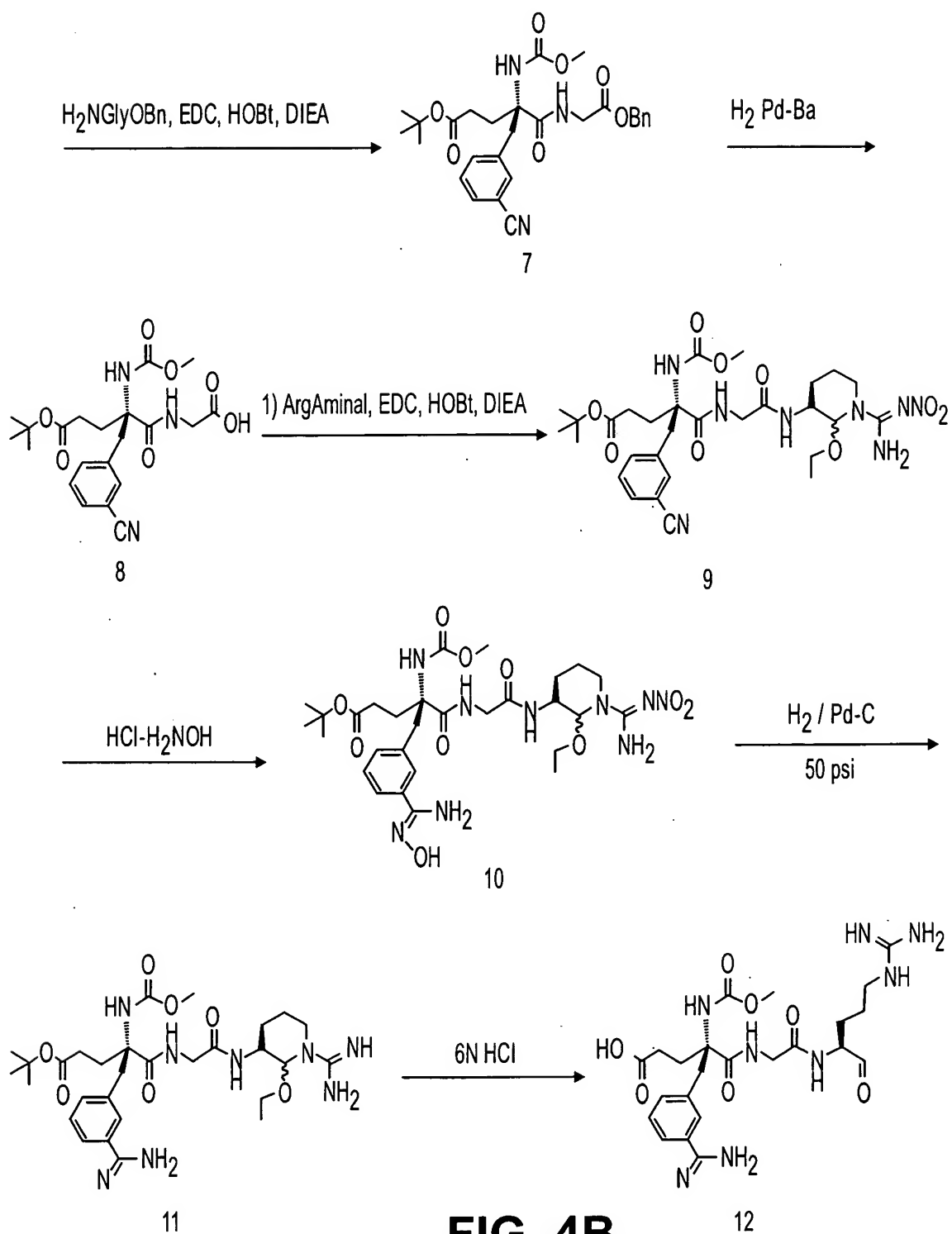


FIG. 4B

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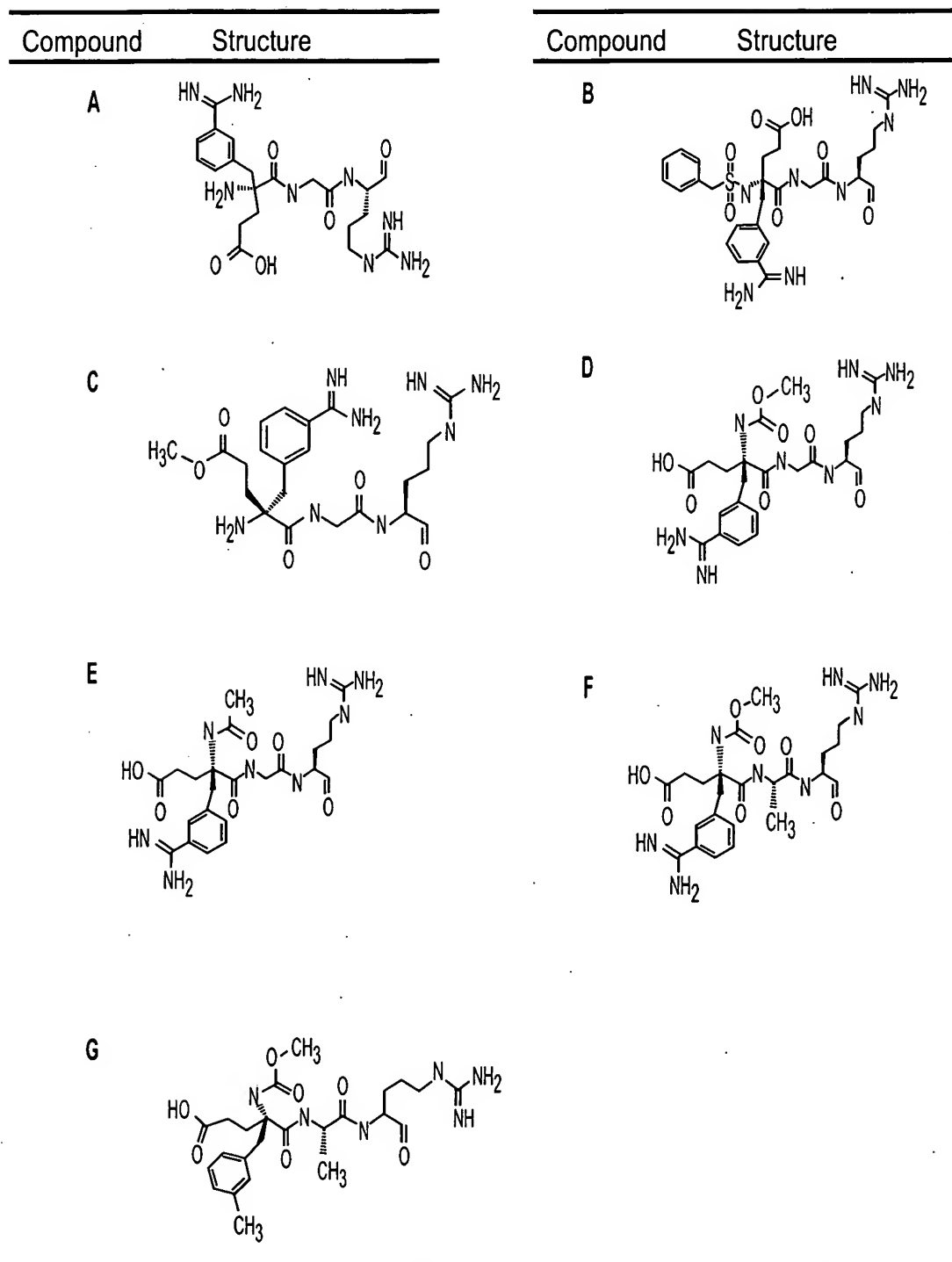


FIG. 5A

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Compound	Structure	Compound	Structure
H		I	
J		K	
L		M	

FIG. 5B